

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/571,511
Source: IFWP
Date Processed by STIC: 3/21/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/571,571

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 J Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/571,511

DATE: 03/21/2006

TIME: 14:09:12

Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

3 <110> APPLICANT: HuBit Genomix, Inc.
 4 Doi, Toshio
 6 <120> TITLE OF INVENTION: A method for detecting diabetic nephropathy and kits
 7 therefor, agents for preventing and/or treating
 8 diabetic nephropathy, a method for identifying
 9 substances effective in prevention and/or treatment
 10 and kits therefor
 12 <130> FILE REFERENCE: FP-039PCT
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/571,511
 C--> 15 <141> CURRENT FILING DATE: 2006-03-10
 17 <150> PRIOR APPLICATION NUMBER: JP P2003-319538
 18 <151> PRIOR FILING DATE: 2003-09-11
 20 <160> NUMBER OF SEQ ID NOS: 24
 22 <170> SOFTWARE: PatentIn Ver. 2.1

*see item 4
on Error Summary
Sheet*

ERRORED SEQUENCES

24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1990
 E--> 26 <212> TYPE: mRNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (433)..(1830)
 33 <400> SEQUENCE: 1

This is not an RNA sequence

**Does Not Comply
Corrected Diskette Needed**

invalid response.

*Per sequence rules, the
only valid <212> responses are: DNA, PRT, or
RNA*

34 gaattccggg ggtattggca gctgaggagt ggaggtctggg cagctccgac tccctgacgc 60
 36 cagcgcgacc agatcaatcc aggtccagg agaaagcagg cgggcgggcg gagaaaggag 120
 38 aggccgagcg gctcaaccgc ggccgaggct cggggagcgg agagtggcgc accgcccggc 180
 40 cgtccggacc cgggcgcgca gaccccgctc gcccggccac tctgtctccc gcacggacgg 240
 42 gcgcgcgcgc aacccgggtgc tgactgggtt acttttttaa acactaggaa tggtaatttc 300
 44 tactcttctg gacttcaaac taagaagtta aagagacttc tctgtaaata aacaaatctc 360
 46 ttctgtgtgc cttttgcatt tggagacagc tttatttcac catatccaag gagtataact 420
 48 agtgtgtgca tt atg aat gtg aca agt tta ttt tcc ttt aca agt cca gct 471
 49 Met Asn Val Thr Ser Leu Phe Ser Phe Thr Ser Pro Ala
 50 1 5 10
 52 gtg aag aga ctt ctt ggg tgg aaa cag ggc gat gaa gaa gaa aaa tgg 519
 53 Val Lys Arg Leu Leu Gly Trp Lys Gln Gly Asp Glu Glu Glu Lys Trp
 54 15 20 25
 56 gca gag aaa gct gtt gat gct ttg gtg aaa aaa ctg aag aaa aag aaa 567
 57 Ala Glu Lys Ala Val Asp Ala Leu Val Lys Lys Leu Lys Lys Lys Lys
 58 30 35 40 45
 60 ggt gcc atg gag gaa ctg gaa aag gcc ttg agc tgc cca ggg caa ccg 615

*For a combined
DNA/RNA
sequence, use
<212> DNA and
explain in
<220>-<223>
section.*

*Explain any
modifications in
<220>-<223> section (on
3/21/2006)*

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Input Set : A:\PTO.TS..txt

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61	Gly	Ala	Met	Glu	Glu	Leu	Glu	Lys	Ala	Leu	Ser	Cys	Pro	Gly	Gln	Pro	
62					50					55					60		
64	agt	aac	tgt	gtc	acc	att	ccc	cgc	tct	ctg	gat	ggc	agg	ctg	caa	gtc	663
65	Ser	Asn	Cys	Val	Thr	Ile	Pro	Arg	Ser	Leu	Asp	Gly	Arg	Leu	Gln	Val	
66				65					70					75			
68	tcc	cac	cgg	aag	gga	ctg	cct	cat	gtc	att	tac	tgc	cgt	gtg	tgg	cgc	711
69	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr	Cys	Arg	Val	Trp	Arg	
70				80				85					90				
72	tgg	ccc	gat	ctt	cag	agc	cac	cat	gaa	cta	aaa	cca	ctg	gaa	tgc	tgt	759
73	Trp	Pro	Asp	Leu	Gln	Ser	His	His	Glu	Leu	Lys	Pro	Leu	Glu	Cys	Cys	
74			95				100					105					
76	gag	ttt	cct	ttt	ggt	tcc	aag	cag	aag	gag	gtc	tgc	atc	aat	ccc	tac	807
77	Glu	Phe	Pro	Phe	Gly	Ser	Lys	Gln	Lys	Glu	Val	Cys	Ile	Asn	Pro	Tyr	
78	110					115					120				125		
80	cac	tat	aag	aga	gta	gaa	agc	cct	gta	ctt	cct	cct	gtg	ctg	gtt	cca	855
81	His	Tyr	Lys	Arg	Val	Glu	Ser	Pro	Val	Leu	Pro	Pro	Val	Leu	Val	Pro	
82					130					135					140		
84	aga	cac	agc	gaa	tat	aat	cct	cag	cac	agc	ctc	tta	gct	cag	ttc	cgt	903
85	Arg	His	Ser	Glu	Tyr	Asn	Pro	Gln	His	Ser	Leu	Leu	Ala	Gln	Phe	Arg	
86				145				150					155				
88	aac	tta	gga	caa	aat	gag	cct	cac	atg	cca	ctc	aac	gcc	act	ttt	cca	951
89	Asn	Leu	Gly	Gln	Asn	Glu	Pro	His	Met	Pro	Leu	Asn	Ala	Thr	Phe	Pro	
90			160					165					170				
92	gat	tct	ttc	cag	caa	ccc	aac	agc	cac	ccg	ttt	cct	cac	tct	ccc	aat	999
93	Asp	Ser	Phe	Gln	Gln	Pro	Asn	Ser	His	Pro	Phe	Pro	His	Ser	Pro	Asn	
94			175				180					185					
96	agc	agt	tac	cca	aac	tct	cct	ggg	agc	agc	agc	agc	acc	tac	cct	cac	1047
97	Ser	Ser	Tyr	Pro	Asn	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Thr	Tyr	Pro	His	
98	190					195				200				205			
100	tct	ccc	acc	agc	tca	gac	cca	gga	agc	cct	ttc	cag	atg	cca	gct	gat	1095
101	Ser	Pro	Thr	Ser	Ser	Asp	Pro	Gly	Ser	Pro	Phe	Gln	Met	Pro	Ala	Asp	
102					210					215				220			
104	acg	ccc	cca	cct	gct	tac	ctg	cct	cct	gaa	gac	ccc	atg	acc	cag	gat	1143
105	Thr	Pro	Pro	Pro	Ala	Tyr	Leu	Pro	Pro	Glu	Asp	Pro	Met	Thr	Gln	Asp	
106				225				230				235					
108	ggc	tct	cag	ccg	atg	gac	aca	aac	atg	atg	gcg	cct	ccc	ctg	ccc	tca	1191
109	Gly	Ser	Gln	Pro	Met	Asp	Thr	Asn	Met	Met	Ala	Pro	Pro	Leu	Pro	Ser	
110			240					245				250					
112	gaa	atc	aac	aga	gga	gat	gtt	cag	gcg	gtt	gct	tat	gag	gaa	cca	aaa	1239
113	Glu	Ile	Asn	Arg	Gly	Asp	Val	Gln	Ala	Val	Ala	Tyr	Glu	Glu	Pro	Lys	
114			255				260					265					
116	cac	tgg	tgc	tct	att	gtc	tac	tat	gag	ctc	aac	aat	cgt	gtg	ggt	gaa	1287
117	His	Trp	Cys	Ser	Ile	Val	Tyr	Tyr	Glu	Leu	Asn	Asn	Arg	Val	Gly	Glu	
118	270					275				280				285			
120	gcg	ttc	cat	gcc	tcc	tcc	aca	agt	gtg	ttg	gtg	gat	ggt	ttc	act	gat	1335
121	Ala	Phe	His	Ala	Ser	Ser	Thr	Ser	Val	Leu	Val	Asp	Gly	Phe	Thr	Asp	
122					290					295				300			
124	cct	tcc	aac	aat	aag	aac	cgt	ttc	tgc	ctt	ggg	ctg	ctc	tcc	aat	gtt	1383
125	Pro	Ser	Asn	Asn	Lys	Asn	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	

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126          305          310          315
128 aac cgg aat tcc act att gaa aac acc agg cgg cat att gga aaa gga 1431
129 Asn Arg Asn Ser Thr Ile Glu Asn Thr Arg Arg His Ile Gly Lys Gly
130          320          325          330
132 gtt cat ctt tat tat gtt gga ggg gag gtg tat gcc gaa tgc ctt agt 1479
133 Val His Leu Tyr Tyr Val Gly Gly Glu Val Tyr Ala Glu Cys Leu Ser
134          335          340          345
136 gac agt agc atc ttt gtg caa agt cgg aac tgc aac tac cat cat gga 1527
137 Asp Ser Ser Ile Phe Val Gln Ser Arg Asn Cys Asn Tyr His His Gly
138 350          355          360          365
140 ttt cat cct act act gtt tgc aag atc cct agt ggg tgt agt ctg aaa 1575
141 Phe His Pro Thr Thr Val Cys Lys Ile Pro Ser Gly Cys Ser Leu Lys
142          370          375          380
144 att ttt aac aac caa gaa ttt gct cag tta ttg gca cag tct gtg aac 1623
145 Ile Phe Asn Asn Gln Glu Phe Ala Gln Leu Leu Ala Gln Ser Val Asn
146          385          390          395
148 cat gga ttt gag aca gtc tat gag ctt aca aaa atg tgt act ata cgt 1671
149 His Gly Phe Glu Thr Val Tyr Glu Leu Thr Lys Met Cys Thr Ile Arg
150          400          405          410
152 atg agc ttt gtg aag ggc tgg gga gca gaa tac cac cgc cag gat gtt 1719
153 Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr His Arg Gln Asp Val
154          415          420          425
156 act agc acc ccc tgc tgg att gag ata cat ctg cac ggc ccc ctc cag 1767
157 Thr Ser Thr Pro Cys Trp Ile Glu Ile His Leu His Gly Pro Leu Gln
158 430          435          440          445
160 tgg ctg gat aaa gtt ctt act caa atg ggt tca cct cat aat cct att 1815
161 Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro His Asn Pro Ile
162          450          455          460
164 tca tct gta tct taa atggccccag catctgcctc tggaaaacta ttgagccttg 1870
165 Ser Ser Val Ser
166          465
168 catgtacttg aaggatggat gagtcagaca cgattgagaa ctgacaaagg agccttgata 1930
170 atacttgacc tctgtgacca actgttggat tcagaaattt aaacaaaaaa aaaaaaaaaa 1990
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 1970
E--> 175 <212> TYPE: mRNA same env
176 <213> ORGANISM: Homo sapiens
178 <220> FEATURE:
179 <221> NAME/KEY: CDS
180 <222> LOCATION: (283)..(1794)
182 <400> SEQUENCE: 2
183 aggaaacggt ttattaggag ggagtggtgg agctggggcca ggcaggaaga cgctggaata 60
185 agaaacattt ttgtccagc ccccatccca gtcccgaggag gctgccgcgc cagctgcgcc 120
187 gagcgagccc ctccccggt ccagcccggg ccggggccgc gccggacccc agcccgcgt 180
189 ccagcgctgg cgggtgcaact gcggccgcgc ggtggagggg aggtggcccc ggtccgccga 240
191 aggctagcgc cccgccaccc gcagagcggg cccagaggga cc atg acc ttg ggc 294
192          Met Thr Leu Gly
193          1
195 tcc ccc agg aaa ggc ctt ctg atg ctg ctg atg gcc ttg gtg acc cag 342

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196	Ser	Pro	Arg	Lys	Gly	Leu	Leu	Met	Leu	Leu	Met	Ala	Leu	Val	Thr	Gln	
197	5					10					15					20	
199	gga	gac	cct	gtg	aag	ccg	tct	cgg	ggc	ccg	ctg	gtg	acc	tgc	acg	tgt	390
200	Gly	Asp	Pro	Val	Lys	Pro	Ser	Arg	Gly	Pro	Leu	Val	Thr	Cys	Thr	Cys	
201					25					30					35		
203	gag	agc	cca	cat	tgc	aag	ggg	cct	acc	tgc	cgg	ggg	gcc	tgg	tgc	aca	438
204	Glu	Ser	Pro	His	Cys	Lys	Gly	Pro	Thr	Cys	Arg	Gly	Ala	Trp	Cys	Thr	
205				40					45					50			
207	gta	gtg	ctg	gtg	cgg	gag	gag	ggg	agg	cac	ccc	cag	gaa	cat	cgg	ggc	486
208	Val	Val	Leu	Val	Arg	Glu	Glu	Gly	Arg	His	Pro	Gln	Glu	His	Arg	Gly	
209				55				60						65			
211	tgc	ggg	aac	ttg	cac	agg	gag	ctc	tgc	agg	ggg	cgc	ccc	acc	gag	ttc	534
212	Cys	Gly	Asn	Leu	His	Arg	Glu	Leu	Cys	Arg	Gly	Arg	Pro	Thr	Glu	Phe	
213		70					75					80					
215	gtc	aac	cac	tac	tgc	tgc	gac	agc	cac	ctc	tgc	aac	cac	aac	gtg	tcc	582
216	Val	Asn	His	Tyr	Cys	Cys	Asp	Ser	His	Leu	Cys	Asn	His	Asn	Val	Ser	
217	85					90					95					100	
219	ctg	gtg	ctg	gag	gcc	acc	caa	cct	cct	tcg	gag	cag	ccg	gga	aca	gat	630
220	Leu	Val	Leu	Glu	Ala	Thr	Gln	Pro	Pro	Ser	Glu	Gln	Pro	Gly	Thr	Asp	
221					105					110					115		
223	ggc	cag	ctg	gcc	ctg	atc	ctg	ggc	ccc	gtg	ctg	gcc	ttg	ctg	gcc	ctg	678
224	Gly	Gln	Leu	Ala	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	Leu	Ala	Leu	
225				120					125					130			
227	gtg	gcc	ctg	ggt	gtc	ctg	ggc	ctg	tgg	cat	gtc	cga	cgg	agg	cag	gag	726
228	Val	Ala	Leu	Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg	Arg	Arg	Gln	Glu	
229				135				140						145			
231	aag	cag	cgt	ggc	ctg	cac	agc	gag	ctg	gga	gag	tcc	agt	ctc	atc	ctg	774
232	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	Ser	Leu	Ile	Leu	
233		150					155					160					
235	aaa	gca	tct	gag	cag	ggc	gac	acg	atg	ttg	ggg	gac	ctc	ctg	gac	agt	822
236	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	Leu	Leu	Asp	Ser	
237	165					170					175					180	
239	gac	tgc	acc	aca	ggg	agt	ggc	tca	ggg	ctc	ccc	ttc	ctg	gtg	cag	agg	870
240	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	
241					185					190					195		
243	aca	gtg	gca	cgg	cag	gtt	gcc	ttg	gtg	gag	tgt	gtg	gga	aaa	ggc	cgc	918
244	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	Lys	Gly	Arg	
245				200						205					210		
247	tat	ggc	gaa	gtg	tgg	cgg	ggc	ttg	tgg	cac	ggt	gag	agt	gtg	gcc	gtc	966
248	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	Ser	Val	Ala	Val	
249			215					220						225			
251	aag	atc	ttc	tcc	tcg	agg	gat	gaa	cag	tcc	tgg	ttc	cgg	gag	act	gag	1014
252	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	Glu	Thr	Glu	
253		230					235					240					
255	atc	tat	aac	aca	gta	ttg	ctc	aga	cac	gac	aac	atc	cta	ggc	ttc	atc	1062
256	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	Gly	Phe	Ile	
257	245					250					255					260	
259	gcc	tca	gac	atg	acc	tcc	cgc	aac	tcg	agc	acg	cag	ctg	tgg	ctc	atc	1110
260	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	

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261          265          270          275
263 acg cac tac cac gag cac ggc tcc ctc tac gac ttt ctg cag aga cag 1158
264 Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln
265          280          285          290
267 acg ctg gag ccc cat ctg gct ctg agg cta gct gtg tcc gcg gca tgc 1206
268 Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys
269          295          300          305
271 ggc ctg gcg cac ctg cac gtg gag atc ttc ggt aca cag ggc aaa cca 1254
272 Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro
273          310          315          320
275 gcc att gcc cac cgc gac ttc aag agc cgc aat gtg ctg gtc aag agc 1302
276 Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser
277 325          330          335          340
279 aac ctg cag tgt tgc atc gcc gac ctg ggc ctg gct gtg atg cac tca 1350
280 Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser
281          345          350          355
283 cag ggc agc gat tac ctg gac atc ggc aac aac ccg aga gtg ggc acc 1398
284 Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr
285          360          365          370
287 aag cgg tac atg gca ccc gag gtg ctg gac gag cag atc cgc acg gac 1446
288 Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
289          375          380          385
291 tgc ttt gag tcc tac aag tgg act gac atc tgg gcc ttt ggc ctg gtg 1494
292 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
293          390          395          400
295 ctg tgg gag att gcc cgc cgg acc atc gtg aat ggc atc gtg gag gac 1542
296 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
297 405          410          415          420
299 tat aga cca ccc ttc tat gat gtg gtg ccc aat gac ccc agc ttt gag 1590
300 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
301          425          430          435
303 gac atg aag aag gtg gtg tgt gtg gat cag cag acc ccc acc atc cct 1638
304 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
305          440          445          450
307 aac cgg ctg gct gca gac ccg gtc ctc tca ggc cta gct cag atg atg 1686
308 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
309          455          460          465
311 cgg gag tgc tgg tac cca aac ccc tct gcc cga ctc acc gcg ctg cgg 1734
312 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
313          470          475          480
315 atc aag aag aca cta caa aaa att agc aac agt cca gag aag cct aaa 1782
316 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
317 485          490          495          500
319 gtg att caa tag ccaggagca cctgattcct ttctgcctgc agggggctgg 1834
320 Val Ile Gln
322 ggggggtgggg ggcagtggat ggtgccctat ctgggtagag gtagtgtgag tgtggtgtgt 1894
324 gctgggggatg ggcagctgcg cctgcctgct cggccccag cccaccagc caaaaataca 1954
326 gctgggctga aacctg 1970
329 <210> SEQ ID NO: 3

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330 <211> LENGTH: 1547
E--> 331 <212> TYPE: mRNA same
332 <213> ORGANISM: Homo sapiens
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (324)..(1514)
338 <400> SEQUENCE: 3
339 ggggacttct tgaacttgca gggagaataa cttgcgccacc ccactttgcg ccggtgcctt 60
341 tgccccagcg gagcctgctt cgccatctcc gagccccacc gcccctccac tcctcggcct 120
343 tgcccgacac tgagacgctg ttcccagcgt gaaaagagag actgcgcggc cggcaccggg 180
345 gagaaggagg aggcaaagaa aaggaacgga cattcggtcc ttgcgccagg tcctttgacc 240
347 agagtttttc catgtggacg ctctttcaat ggacgtgtcc ccgcgtgctt cttagacgga 300
349 ctgcggtctc ctaaaggteg acc atg gtg gcc ggg acc cgc tgt ctt cta gcg 353
350 Met Val Ala Gly Thr Arg Cys Leu Leu Ala
351 1 5 10
353 ttg ctg ctt ccc cag gtc ctc ctg ggc ggc gcg gct ggc ctc gtt ccg 401
354 Leu Leu Leu Pro Gln Val Leu Leu Gly Gly Ala Ala Gly Leu Val Pro
355 15 20 25
357 gag ctg ggc cgc agg aag ttc gcg gcg gcg tcg tcg ggc cgc ccc tca 449
358 Glu Leu Gly Arg Arg Lys Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser
359 30 35 40
361 tcc cag ccc tct gac gag gtc ctg agc gag ttc gag ttg cgg ctg ctc 497
362 Ser Gln Pro Ser Asp Glu Val Leu Ser Glu Phe Glu Leu Arg Leu Leu
363 45 50 55
365 agc atg ttc ggc ctg aaa cag aga ccc acc ccc agc agg gac gcc gtg 545
366 Ser Met Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser Arg Asp Ala Val
367 60 65 70
369 gtg ccc ccc tac atg cta gac ctg tat cgc agg cac tca ggt cag ccg 593
370 Val Pro Pro Tyr Met Leu Asp Leu Tyr Arg Arg His Ser Gly Gln Pro
371 75 80 85 90
373 ggc tca ccc gcc cca gac cac cgg ttg gag agg gca gcc agc cga gcc 641
374 Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala
375 95 100 105
377 aac act gtg cgc agc ttc cac cat gaa gaa tct ttg gaa gaa cta cca 689
378 Asn Thr Val Arg Ser Phe His His Glu Glu Ser Leu Glu Glu Leu Pro
379 110 115 120
381 gaa acg agt ggg aaa aca acc cgg aga ttc ttc ttt aat tta agt tct 737
382 Glu Thr Ser Gly Lys Thr Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser
383 125 130 135
385 atc ccc acg gag gag ttt atc acc tca gca gag ctt cag gtt ttc cga 785
386 Ile Pro Thr Glu Glu Phe Ile Thr Ser Ala Glu Leu Gln Val Phe Arg
387 140 145 150
389 gaa cag atg caa gat gct tta gga aac aat agc agt ttc cat cac cga 833
390 Glu Gln Met Gln Asp Ala Leu Gly Asn Asn Ser Ser Phe His His Arg
391 155 160 165 170
393 att aat att tat gaa atc ata aaa cct gca aca gcc aac tcg aaa ttc 881
394 Ile Asn Ile Tyr Glu Ile Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe
395 175 180 185
397 ccc gtg acc aga ctt ttg gac acc agg ttg gtg aat cag aat gca agc 929

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398 Pro Val Thr Arg Leu Leu Asp Thr Arg Leu Val Asn Gln Asn Ala Ser
399          190          195          200
401 agg tgg gaa agt ttt gat gtc acc ccc gct gtg atg cgg tgg act gca 977
402 Arg Trp Glu Ser Phe Asp Val Thr Pro Ala Val Met Arg Trp Thr Ala
403          205          210          215
405 cag gga cac gcc aac cat gga ttc gtg gtg gaa gtg gcc cac ttg gag 1025
406 Gln Gly His Ala Asn His Gly Phe Val Val Glu Val Ala His Leu Glu
407          220          225          230
409 gag aaa caa ggt gtc tcc aag aga cat gtt agg ata agc agg tct ttg 1073
410 Glu Lys Gln Gly Val Ser Lys Arg His Val Arg Ile Ser Arg Ser Leu
411 235          240          245          250
413 cac caa gat gaa cac agc tgg tca cag ata agg cca ttg cta gta act 1121
414 His Gln Asp Glu His Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr
415          255          260          265
417 ttt ggc cat gat gga aaa ggg cat cct ctc cac aaa aga gaa aaa cgt 1169
418 Phe Gly His Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg
419          270          275          280
421 caa gcc aaa cac aaa cag cgg aaa cgc ctt aag tcc agc tgt aag aga 1217
422 Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg
423          285          290          295
425 cac cct ttg tac gtg gac ttc agt gac gtg ggg tgg aat gac tgg att 1265
426 His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile
427          300          305          310
429 gtg gct ccc ccg ggg tat cac gcc ttt tac tgc cac gga gaa tgc cct 1313
430 Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro
431 315          320          325          330
433 ttt cct ctg gct gat cat ctg aac tcc act aat cat gcc att gtt cag 1361
434 Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln
435          335          340          345
437 acg ttg gtc aac tct gtt aac tct aag att cct aag gca tgc tgt gtc 1409
438 Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val
439          350          355          360
441 ccg aca gaa ctc agt gct atc tcg atg ctg tac ctt gac gag aat gaa 1457
442 Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu
443          365          370          375
445 aag gtt gta tta aag aac tat cag gac atg gtt gtg gag ggt tgt ggg 1505
446 Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
447          380          385          390
449 tgt cgc tag tacagcaaaa ttaaatacat aaatatatat ata 1547
450 Cys Arg
451 395

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454 <210> SEQ ID NO: 4

455 <211> LENGTH: 1999

E--> 456 <212> TYPE: mRNA

457 <213> ORGANISM: Homo sapiens

459 <220> FEATURE:

460 <221> NAME/KEY: CDS

461 <222> LOCATION: (478)..(1704)

463 <400> SEQUENCE: 4

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Input Set : A:\PTO.TS..txt

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464 gagggagggg ccgccgggga agaggaggag gaaggaaaga aagaaagcga gggagggaaa 60
466 gaggaggaag gaagatgcga gaaggcagag gagggaggag ggaggggaagg agcgcgagagc 120
468 ccggcccga agctaggtga gtgtggcatc cgagctgagg gacgcgagcc tgagacgccg 180
470 ctgctgctcc ggctgagtat ctagcttgct tccccgatgg gattccccgtc caagctatct 240
472 cgagcctgca gcgccacagt ccccgccctt cgcccagggt cactgcaacc gttcagaggt 300
474 ccccaggagc tgctgctggc gagcccgtta ctgcagggac ctatggagcc attccgtagt 360
476 gccatcccga gcaacgcact gctgcagctt ccctgagcct ttccagcaag tttgttcaag 420
478 attggctgtc aagaatcatg gactgttatt atatgccttg ttttctgtca agacacc 477
480 atg att cct ggt aac cga atg ctg atg gtc gtt tta tta tgc caa gtc 525
481 Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
482 1 5 10 15
484 ctg cta gga ggc gcg agc cat gct agt ttg ata cct gag acg ggg aag 573
485 Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
486 20 25 30
488 aaa aaa gtc gcc gag att cag ggc cac gcg gga gga cgc cgc tca ggg 621
489 Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
490 35 40 45
492 cag agc cat gag ctc ctg cgg gac ttc gag gcg aca ctt ctg cag atg 669
493 Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
494 50 55 60
496 ttt ggg ctg cgc cgc cgc ccg cag cct agc aag agt gcc gtc att ccg 717
497 Phe Gly Leu Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
498 65 70 75 80
500 gac tac atg cgg gat ctt tac cgg ctt cag tct ggg gag gag gag gaa 765
501 Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
502 85 90 95
504 gag cag atc cac agc act ggt ctt gag tat cct gag cgc ccg gcc agc 813
505 Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
506 100 105 110
508 cgg gcc aac acc gtg agg agc ttc cac cac gaa gaa cat ctg gag aac 861
509 Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
510 115 120 125
512 atc cca ggg acc agt gaa aac tct gct ttt cgt ttc ctc ttt aac ctc 909
513 Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
514 130 135 140
516 agc agc atc cct gag aac gag gcg atc tcc tct gca gag ctt cgg ctc 957
517 Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu
518 145 150 155 160
520 ttc cgg gag cag gtg gac cag ggc cct gat tgg gaa agg ggc ttc cac 1005
521 Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
522 165 170 175
524 cgt ata aac att tat gag gtt atg aag ccc cca gca gaa gtg gtg cct 1053
525 Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
526 180 185 190
528 ggg cac ctc atc aca cga cta ctg gac acg aga ctg gtc cac cac aat 1101
529 Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
530 195 200 205
532 gtg aca cgg tgg gaa act ttt gat gtg agc cct gcg gtc ctt cgc tgg 1149
533 Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp

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Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

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534      210      215      220
536 acc cgg gag aag cag cca aac tat ggg cta gcc att gag gtg act cac 1197
537 Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
538 225      230      235      240
540 ctc cat cag act cgg acc cac cag ggc cag cat gtc agg att agc cga 1245
541 Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
542      245      250      255
544 tcg tta cct caa ggg agt ggg aat tgg gcc cag ctc cgg ccc ctc ctg 1293
545 Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
546      260      265      270
548 gtc acc ttt ggc cat gat ggc cgg ggc cat gcc ttg acc cga cgc cgg 1341
549 Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
550      275      280      285
552 agg gcc aag cgt agc cct aag cat cac tca cag cgg gcc agg aag aag 1389
553 Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
554      290      295      300
556 aat aag aac tgc cgg cgc cac tcg ctc tat gtg gac ttc agc gat gtg 1437
557 Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
558 305      310      315      320
560 ggc tgg aat gac tgg att gtg gcc cca cca ggc tac cag gcc ttc tac 1485
561 Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
562      325      330      335
564 tgc cat ggg gac tgc ccc ttt cca ctg gct gac cac ctc aac tca acc 1533
565 Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
566      340      345      350
568 aac cat gcc att gtg cag acc ctg gtc aat tct gtc aat tcc agt atc 1581
569 Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
570      355      360      365
572 ccc aaa gcc tgt tgt gtg ccc act gaa ctg agt gcc atc tcc atg ctg 1629
573 Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
574      370      375      380
576 tac ctg gat gag tat gat aag gtg gta ctg aaa aat tat cag gag atg 1677
577 Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
578 385      390      395      400
580 gta gta gag gga tgt ggg tgc cgc tga gatcaggcag tccttgagga 1724
581 Val Val Glu Gly Cys Gly Cys Arg
582      405
584 tagacagata tacacaccac acacacacac cacatacacc acacacacac gttcccatcc 1784
586 actcaccacac acactacaca gactgcttcc ttatagctgg acttttatTTT aaaaaaaaaa 1844
588 aaaaaaaaaaT ggaaaaaatc cctaaacatt caccttgacc ttatttatga ctttacgtgc 1904
590 aaatgtttttg accatatattga tcatatatTTT tgacaaaaata tattttataac tacgtattaa 1964
592 aagaaaaaaaT taaaatgagt cattattttta aaggt 1999
763 <210> SEQ ID NO: 19
764 <211> LENGTH: 4978
E--> 765 <212> TYPE: mRNA
766 <213> ORGANISM: Homo sapiens
768 <220> FEATURE:
769 <221> NAME/KEY: CDS
770 <222> LOCATION: (241)..(2553)

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772 <400> SEQUENCE: 19

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773 ggtttccgga gctgcggcgg cgcagactgg gaggggggagc cggggggttcc gacgtcgcag 60
775 ccgaggggaac aagccccaac cggatcctgg acaggcacc cggcttggcg ctgtctctcc 120
777 ccctcggctc ggagaggccc ttcggcctga gggagcctcg ccgcccgtcc ccggcacacg 180
779 cgcagccccg gcctctcggc ctctgccgga gaaacagttg ggaccctga ttttagcagg 240
781 atg gcc caa tgg aat cag cta cag cag ctt gac aca cgg tac ctg gag 288
782 Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr Leu Glu
783 1 5 10 15
785 cag ctc cat cag ctc tac agt gac agc ttc cca atg gag ctg cgg cag 336
786 Gln Leu His Gln Leu Tyr Ser Asp Ser Phe Pro Met Glu Leu Arg Gln
787 20 25 30
789 ttt ctg gcc cct tgg att gag agt caa gat tgg gca tat gcg gcc agc 384
790 Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser
791 35 40 45
793 aaa gaa tca cat gcc act ttg gtg ttt cat aat ctc ctg gga gag att 432
794 Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile
795 50 55 60
797 gac cag cag tat agc cgc ttc ctg caa gag tcg aat gtt ctc tat cag 480
798 Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln
799 65 70 75 80
801 cac aat cta cga aga atc aag cag ttt ctt cag agc agg tat ctt gag 528
802 His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu
803 85 90 95
805 aag cca atg gag att gcc cgg att gtg gcc cgg tgc ctg tgg gaa gaa 576
806 Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu
807 100 105 110
809 tca cgc ctt cta cag act gca gcc act gcg gcc cag caa ggg ggc cag 624
810 Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln
811 115 120 125
813 gcc aac cac ccc aca gca gcc gtg gtg acg gag aag cag cag atg ctg 672
814 Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu
815 130 135 140
817 gag cag cac ctt cag gat gtc cgg aag aga gtg cag gat cta gaa cag 720
818 Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu Glu Gln
819 145 150 155 160
821 aaa atg aaa gtg gta gag aat ctc cag gat gac ttt gat ttc aac tat 768
822 Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe Asn Tyr
823 165 170 175
825 aaa acc ctc aag agt caa gga gac atg caa gat ctg aat gga aac aac 816
826 Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn
827 180 185 190
829 cag tca gtg acc agg cag aag atg cag cag ctg gaa cag atg ctc act 864
830 Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
831 195 200 205
833 gcg ctg gac cag atg cgg aga agc atc gtg agt gag ctg gcg ggg ctt 912
834 Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
835 210 215 220
837 ttg tca gcg atg gag tac gtg cag aaa act ctc acg gac gag gag ctg 960
838 Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu

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839	225		230		235		240	
841	gct gac tgg aag agg cgg caa cag att gcc tgc att gga ggc ccg ccc	1008						
842	Ala Asp Trp Lys Arg Arg Gln Gln Ile Ala Cys Ile Gly Gly Pro Pro							
843			245		250		255	
845	aac atc tgc cta gat cgg cta gaa aac tgg ata acg tca tta gca gaa	1056						
846	Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu							
847			260		265		270	
849	tct caa ctt cag acc cgt caa caa att aag aaa ctg gag gag ttg cag	1104						
850	Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln							
851			275		280		285	
853	caa aaa gtt tcc tac aaa ggg gac ccc att gta cag cac cgg ccg atg	1152						
854	Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met							
855			290		295		300	
857	ctg gag gag aga atc gtg gag ctg ttt aga aac tta atg aaa agt gcc	1200						
858	Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala							
859	305		310		315		320	
861	ttt gtg gtg gag cgg cag ccc tgc atg ccc atg cat cct gac cgg ccc	1248						
862	Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro							
863			325		330		335	
865	ctc gtc atc aag acc ggc gtc cag ttc act act aaa gtc agg ttg ctg	1296						
866	Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu							
867			340		345		350	
869	gtc aaa ttc cct gag ttg aat tat cag ctt aaa att aaa gtg tgc att	1344						
870	Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile							
871			355		360		365	
873	gac aaa gac tct ggg gac gtt gca gct ctc aga gga tcc cgg aaa ttt	1392						
874	Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe							
875			370		375		380	
877	aac att ctg ggc aca aac aca aaa gtg atg aac atg gaa gaa tcc aac	1440						
878	Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn							
879	385		390		395		400	
881	aac ggc agc ctc tct gca gaa ttc aaa cac ttg acc ctg agg gag cag	1488						
882	Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln							
883			405		410		415	
885	aga tgt ggg aat ggg ggc cga gcc aat tgt gat gct tcc ctg att gtg	1536						
886	Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val							
887			420		425		430	
889	act gag gag ctg cac ctg atc acc ttt gag acc gag gtg tat cac caa	1584						
890	Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln							
891			435		440		445	
893	ggc ctc aag att gac cta gag acc cac tcc ttg cca gtt gtg gtg atc	1632						
894	Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile							
895			450		455		460	
897	tcc aac atc tgt cag atg cca aat gcc tgg gcg tcc atc ctg tgg tac	1680						
898	Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr							
899	465		470		475		480	
901	aac atg ctg acc aac aat ccc aag aat gta aac ttt ttt acc aag ccc	1728						
902	Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro							
903			485		490		495	

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905 cca att gga acc tgg gat caa gtg gcc gag gtc ctg agc tgg cag ttc 1776
906 Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp Gln Phe
907      500      505      510
909 tcc tcc acc acc aag cga gga ctg agc atc gag cag ctg act aca ctg 1824
910 Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr Thr Leu
911      515      520      525
913 gca gag aaa ctc ttg gga cct ggt gtg aat tat tca ggg tgt cag atc 1872
914 Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys Gln Ile
915      530      535      540
917 aca tgg gct aaa ttt tgc aaa gaa aac atg gct ggc aag ggc ttc tcc 1920
918 Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly Phe Ser
919 545      550      555      560
921 ttc tgg gtc tgg ctg gac aat atc att gac ctt gtg aaa aag tac atc 1968
922 Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys Tyr Ile
923      565      570      575
925 ctg gcc ctt tgg aac gaa ggg tac atc atg ggc ttt atc agt aag gag 2016
926 Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser Lys Glu
927      580      585      590
929 cgg gag cgg gcc atc ttg agc act aag cct cca ggc acc ttc ctg cta 2064
930 Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe Leu Leu
931      595      600      605
933 aga ttc agt gaa agc agc aaa gaa gga ggc gtc act ttc act tgg gtg 2112
934 Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr Trp Val
935      610      615      620
937 gag aag gac atc agc ggt aag acc cag atc cag tcc gtg gaa cca tac 2160
938 Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu Pro Tyr
939 625      630      635      640
941 aca aag cag cag ctg aac aac atg tca ttt gct gaa atc atc atg ggc 2208
942 Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Glu Ile Ile Met Gly
943      645      650      655
945 tat aag atc atg gat gct acc aat atc ctg gtg tct cca ctg gtc tat 2256
946 Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu Val Tyr
947      660      665      670
949 ctc tat cct gac att ccc aag gag gag gca ttc gga aag tat tgt cgg 2304
950 Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr Cys Arg
951      675      680      685
953 cca gag agc cag gag cat cct gaa gct gac cca ggt agc gct gcc cca 2352
954 Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala Ala Pro
955      690      695      700
957 tac ctg aag acc aag ttt atc tgt gtg aca cca acg acc tgc agc aat 2400
958 Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys Ser Asn
959 705      710      715      720
961 acc att gac ctg ccg atg tcc ccc cgc act tta gat tca ttg atg cag 2448
962 Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu Met Gln
963      725      730      735
965 ttt gga aat aat ggt gaa ggt gct gaa ccc tca gca gga ggg cag ttt 2496
966 Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly Gln Phe
967      740      745      750
969 gag tcc ctc acc ttt gac atg gag ttg acc tcg gag tgc gct acc tcc 2544

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RAW SEQUENCE LISTING

DATE: 03/21/2006

PATENT APPLICATION: US/10/571,511

TIME: 14:09:12

Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

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970 Glu Ser Leu Thr Phe Asp Met Glu Leu Thr Ser Glu Cys Ala Thr Ser
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973 ccc atg tga ggagctgaga acggaagctg cagaaagata cgactgaggc      2593
974 Pro Met
975          770
977 gcctacctgc attctgccac ccctcacaca gccaaacccc agatcatctg aaactactaa 2653
979 ctttgtgggtt ccagatTTTT tttaatctcc tacttctgct atctttgagc aatctgggca 2713
981 cttttaaaaa tagagaaatg agtgaatgtg ggtgatctgc ttttatctaa atgcaataa 2773
983 ggatgtgttc tctgagaccc atgatcaggg gatgtggcgg ggggtggcta gagggagaaa 2833
985 aaggaaatgt cttgtgttgt tttgttcccc tgccctcctt tctcagcagc tttttgttat 2893
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989 tgaagcaaaa tgccacaggg cacctatagc tacatactcc tggcattgca ctttttaacc 3013
991 ttgctgacat ccaaatagaa gataggacta tctaagccct aggtttcttt ttaaattaag 3073
993 aaataataac aattaaagg caaaaaacac tgtatcagca tagcctttct gtatttaaga 3133
995 aacttaagca gccgggcatg gtggctcacg cctgtaatcc cagcactttg ggaggccgag 3193
997 gcggatcata aggtcaggag atcaagacca tcctggctaa cacggtgaaa ccccgctct 3253
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1005 aaaaaaaaaa aaagaaactt cagttaacag cctccttggg gctttaagca ttcagcttcc 3493
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1037 cgaccttctc taagatgaac agggttcgcc ccagtcctcc tgcttgagga cagttgatgt 4453
1039 gtcattgcaga gctcttactt ctccagcaac actcttcagt acataataag ctttaactgat 4513
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1047 tggcccataa aagaacaggg tcctcaggcc ctgcccgtt cctgtccact gccccctccc 4753
1049 catccccagc ccagccgagg gaatcccgtg ggttgcttac ctacctataa ggtggtttat 4813
1051 aagctgctgt cctggccact gcattcaaat tccaatgtgt acttcatagt gtaaaaattt 4873
1053 atattattgt gaggtttttt gtcttttttt ttttttttt tttttggtat attgctgtat 4933
1055 ctactttaac ttccagaaat aaacgttata taggaaccgt aaaaa      4978
1058 <210> SEQ ID NO: 20
1059 <211> LENGTH: 3631
E--> 1060 <212> TYPE: mRNA
1061 <213> ORGANISM: Homo sapiens

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Input Set : A:\PTO.TS..txt

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1063 <220> FEATURE:
1064 <221> NAME/KEY: CDS
1065 <222> LOCATION: (549)..(2147)
1067 <400> SEQUENCE: 20
1068 gcggccgctg cagagattgg aatccgcctg ccgggcttgg cgaaggagaa gggaggaggc 60
1070 agggagcgagg agggaggagg gccaaaggcg ggcaggaagg cttaggctcg gcgcgtccgt 120
1072 ccgcgcgcgg cgaagatcgc acggccccgat cgaggggcga ccgggtcggg gccgctgcac 180
1074 gccaaaggcg aaggccgatt cgggccccac ttgccccggg cggctcgccg cggccaccgc 240
1076 ctccgcgcgg agggctggag gatgcgttcc ctggggtccg gacttatgaa aatatgcac 300
1078 agtttaatac tgtcttggaa ttcattgagat ggaagcatag gtcaaagctg tttggagaaa 360
1080 atcagaagta cagttttatc tagccacatc ttggaggagt cgtaagaaag cagtgggagt 420
1082 tgaagtcatt gtcaagtgtc tgcgatcttt tacaagaaaa tctcactgaa tgatagtcac 480
1084 ttaaattggt gaagtagcaa gaccaattat taaagggtgac agtacacagg aacattaca 540
1086 attgaaca atg cct cag cta tac att tac atc aga tta ttg gga gcc tat 590
1087 Met Pro Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr
1088      1          5          10
1090 ttg ttc atc att tct cgt gtt caa gga cag aat ctg gat agt atg ctt 638
1091 Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu
1092 15          20          25          30
1094 cat ggc act ggg atg aaa tca gac tcc gac cag aaa aag tca gaa aat 686
1095 His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn
1096          35          40          45
1098 gga gta acc tta gca cca gag gat acc ttg cct ttt tta aag tgc tat 734
1099 Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr
1100          50          55          60
1102 tgc tca ggg cac tgt cca gat gat gct att aat aac aca tgc ata act 782
1103 Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr
1104          65          70          75
1106 aat gga cat tgc ttt gcc atc ata gaa gaa gat gac cag gga gaa acc 830
1107 Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr
1108          80          85          90
1110 aca tta gct tca ggg tgt atg aaa tat gaa gga tct gat ttt cag tgc 878
1111 Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys
1112 95          100          105          110
1114 aaa gat tct cca aaa gcc cag cta cgc cgg aca ata gaa tgt tgt cgg 926
1115 Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg
1116          115          120          125
1118 acc aat tta tgt aac cag tat ttg caa ccc aca ctg ccc cct gtt gtc 974
1119 Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val
1120          130          135          140
1122 ata ggt ccg ttt ttt gat ggc agc att cga tgg ctg gtt ttg ctc att 1022
1123 Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile
1124          145          150          155
1126 tct atg gct gtc tgc ata att gct atg atc atc ttc tcc agc tgc ttt 1070
1127 Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe
1128          160          165          170
1130 tgt tac aaa cat tat tgc aag agc atc tca agc aga cgt cgt tac aat 1118
1131 Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn
1132 175          180          185          190

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Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

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1135	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	
1136				195					200					205			
1138	aaa	gac	ctt	att	gac	cag	tca	caa	agt	tct	ggg	agg	ggg	tct	gga	cta	1214
1139	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	
1140			210					215					220				
1142	cct	tta	ttg	gtt	cag	cga	act	att	gcc	aaa	cag	att	cag	atg	gtc	cgg	1262
1143	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	
1144			225					230					235				
1146	caa	gtt	ggg	aaa	ggc	cga	tat	gga	gaa	gta	tgg	atg	ggc	aaa	tgg	cgt	1310
1147	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	
1148			240				245					250					
1150	ggc	gaa	aaa	gtg	gcg	gtg	aaa	gta	ttc	ttt	acc	act	gaa	gaa	gcc	agc	1358
1151	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	
1152	255				260						265				270		
1154	tgg	ttt	cga	gaa	aca	gaa	atc	tac	caa	act	gtg	cta	atg	cgc	cat	gaa	1406
1155	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	
1156				275					280					285			
1158	aac	ata	ctt	ggg	ttc	ata	gcg	gca	gac	att	aaa	ggg	aca	ggg	tcc	tgg	1454
1159	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	
1160			290					295					300				
1162	act	cag	ctc	tat	ttg	att	act	gat	tac	cat	gaa	aat	gga	tct	ctc	tat	1502
1163	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	
1164			305				310					315					
1166	gac	ttc	ctg	aaa	tgt	gct	aca	ctg	gac	acc	aga	gcc	ctg	ctt	aaa	ttg	1550
1167	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	
1168			320				325					330					
1170	gct	tat	tca	gct	gcc	tgt	ggg	ctg	tgc	cac	ctg	cac	aca	gaa	att	tat	1598
1171	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	
1172	335				340						345				350		
1174	ggc	acc	caa	gga	aag	ccc	gca	att	gct	cat	cga	gac	cta	aag	agc	aaa	1646
1175	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	
1176				355						360					365		
1178	aac	atc	ctc	atc	aag	aaa	aat	ggg	agt	tgc	tgc	att	gct	gac	ctg	ggc	1694
1179	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	
1180			370					375					380				
1182	ctt	gct	gtt	aaa	ttc	aac	agt	gac	aca	aat	gaa	gtt	gat	gtg	ccc	ttg	1742
1183	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro	Leu	
1184			385					390					395				
1186	aat	acc	agg	gtg	ggc	acc	aaa	cgc	tac	atg	gct	ccc	gaa	gtg	ctg	gac	1790
1187	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	
1188			400				405					410					
1190	gaa	agc	ctg	aac	aaa	aac	cac	ttc	cag	ccc	tac	atc	atg	gct	gac	atc	1838
1191	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe	Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	
1192	415				420						425				430		
1194	tac	agc	ttc	ggc	cta	atc	att	tgg	gag	atg	gct	cgt	cgt	tgt	atc	aca	1886
1195	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp	Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	
1196				435					440				445				
1198	gga	ggg	atc	gtg	gaa	gaa	tac	caa	ttg	cca	tat	tac	aac	atg	gta	ccg	1934

RAW SEQUENCE LISTING

DATE: 03/21/2006

PATENT APPLICATION: US/10/571,511

TIME: 14:09:12

Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

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1203 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg
1204          465          470          475
1206 ttg cgg cca att gtg tct aat cgg tgg aac agt gat gaa tgt cta cga 2030
1207 Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg
1208          480          485          490
1210 gca gtt ttg aag cta atg tca gaa tgc tgg gcc cac aat cca gcc tcc 2078
1211 Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser
1212 495          500          505          510
1214 aga ctc aca gca ttg aga att aag aag acg ctt gcc aag atg gtt gaa 2126
1215 Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu
1216          515          520          525
1218 tcc caa gat gta aaa atc tga tgggttaaacc atcggaggag aaactctaga 2177
1219 Ser Gln Asp Val Lys Ile
1220          530
1222 ctgcaagaac tgtttttacc catggcatgg gtggaattag agtggataa ggatgttaac 2237
1224 ttggttctca gactctttct tcaactacgtg ttcacaggct gctaataatta aacctttcag 2297
1226 tactcttatt aggatacaag ctgggaactt ctaaactt cattctttat atatggacag 2357
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1270 aaaaaaaaaa aaaa 3631

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VERIFICATION SUMMARY

DATE: 03/21/2006

PATENT APPLICATION: US/10/571,511

TIME: 14:09:13

Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:1
L:175 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:2
L:331 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:3
L:456 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:4
L:765 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:19
L:1060 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:20